

SEQUENCE LISTING

<110> Saha, K.

<120> Methods and Materials Relating to CD8-Tropic HIV-1

<130> 28335/37036 US

<150> US 60/258,472

<151> 2000-12-28

<160> 27

<170> PatentIn version 3.1

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His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Ser Pro
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Lys Phe Gly Thr Asn Asn Asn Lys Thr Ile Ile Phe Asn Gln Ser Ser
370 375 380

Gly Gly Asp Pro Glu Ile Thr Met His Thr Phe Asn Cys Gly Gly Glu
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Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asn Ser Thr Trp Ile Arg
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Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
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Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
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Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
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Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
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Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
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Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu
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Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Val Asn
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Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu Asn Thr Ser Val
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Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg
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Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly
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Thr Leu Lys Gln Ile Ala Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
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Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
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Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
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Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly
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Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
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405 410 415

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
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Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
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Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
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<210> 8
 <211> 467
 <212> PRT
 <213> HIV-1

<400> 8

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr
 35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
 50 55 60

Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
 65 70 75 80

Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn
 85 90 95

Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
 100 105 110

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn
 115 120 125

Cys Thr Asn Val Asn Val Thr Asn Leu Lys Asn Glu Thr Asn Thr Asn
 130 135 140

Ser Ser Ser Gly Gly Glu Lys Met Glu Glu Gly Glu Met Lys Asn Cys
 145 150 155 160

Ser Phe Asn Val Thr Thr Leu Ile Arg Asn Lys Arg Lys Thr Glu Tyr
 165 170 175

Ala Leu Phe Tyr Lys Leu Asp Val Met Pro Ile Asp Arg Asp Asn Thr
180 185 190

Ser Tyr Thr Leu Ile Asn Cys Lys Ser Ser Thr Ile Thr Gln Ala Cys
195 200 205

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
210 215 220

Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Lys Gly
225 230 235 240

Pro Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro
245 250 255

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Asp
260 265 270

Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Asn Ile Ile
275 280 285

Val Gln Leu Asn Val Ser Leu Glu Ile Asn Cys Thr Arg Pro Asn Asn
290 295 300

Asn Thr Arg Lys Lys Ile Thr Leu Gly Arg Ser Arg Val Leu Tyr Thr
305 310 315 320

Thr Gly Glu Ile Ile Gly Asp Ile Arg Arg Ala His Cys Asn Leu Ser
325 330 335

Arg Thr Ser Trp Asn Asn Thr Leu Lys Gln Ile Val Glu Lys Leu Arg
340 345 350

Glu Ile Lys Gln Phe Lys Asn Lys Thr Ile Val Phe Lys Gln Ser Ser
355 360 365

Gly Gly Asp Phe Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu
370 375 380

Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp His Ala
385 390 395 400

Asn Gly Thr Trp Lys Asn Thr Glu Gly Ala Asp Asn Asn Ile Thr Leu
405 410 415

Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly Lys
420 425 430

Ala Met Tyr Ala Pro Pro Ile Glu Gly Gln Ile Arg Cys Leu Ser Asn
 435 440 445

Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Ser Glu Glu Asn
 450 455 460

Gln Thr Glu
 465

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 <211> 2553
 <212> DNA
 <213> HIV-1

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 gtcacagttt attatgggggt acctgtgtgg aaagaagcaa ccactactct attttgtgca 180
 tcagatgcta aatcatatga accagaggca cataatatct gggctacaca tgctgtgtg 240
 ccaacagacc ccaaccacg agaaataaaa ctggaaaatg tcacagaaaa ctttaacatg 300
 tggaaaaatg acatggtgga gcagatgcat gaggatgtaa tcagtctatg ggatcaaagc 360
 ctgaaaccat gtgtaaaatt aacccactc tgtgtcactt tacattgcac tgaatataag 420
 gccctaagt ccactattaa tgccactgat agggacatag gaatgaaaaa ctgctctttc 480
 aatgtaacca cagaagtaat aaataagaag aagcaagaac atgcactttt ttataaactt 540
 gatgtggtac aaatggatga taatagtact aataccaact atagattaat aaattgtaat 600
 acctcagtca ttacacaggc gtgtccaaag gtaacctttg agccaattcc catacattat 660
 tgtgctccag ctggatttgc gattctaaag tgtaatgata agaagttcaa tgggacgggt 720
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 aggccctacg aaaataaaag acgacgtaca cctataggac tagggcaagc gtactataca 960
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 gaatttttct actgcgatac atcaagactg tttaatagga cttataatac atcaggtagt 1200
 acaggggtaa ataacagtac aatcaaactc ccatgcagaa taaaacaaat tataaacatg 1260
 tggcagggag taggaaaagc aatgtatgcc cctcccattg aaggactaat caaatgttca 1320
 tcaaacatta caggactatt gttgacaaga gatgggggaa ataatactag gcagaatgaa 1380

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gaaagagaaa aaagagcaat aggactagga gctatgttcc ttgggttctt gggagcagca 1560
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ctaaagaata gtgctattag cttatttgat accacagcaa tagcagtagc tgaggggaca 2460
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<210> 10
 <211> 781
 <212> PRT
 <213> HIV-1

<400> 10
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Gln His Ser Leu Trp Arg Trp Gly Ile Met Leu Leu Gly Met Leu Met
 20 25 30

Ile Cys Lys Gly Glu Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 35 40 45

Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ser
 50 55 60

Tyr Glu Pro Glu Ala His Asn Ile Trp Ala Thr His Ala Cys Val Pro
65 70 75 80

Thr Asp Pro Asn Pro Arg Glu Ile Lys Leu Glu Asn Val Thr Glu Asn
85 90 95

Phe Asn Met Trp Lys Asn Asp Met Val Glu Gln Met His Glu Asp Val
100 105 110

Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
115 120 125

Leu Cys Val Thr Leu His Cys Thr Glu Tyr Lys Ala Pro Asn Ala Thr
130 135 140

Ile Asn Ala Thr Asp Arg Asp Ile Gly Met Lys Asn Cys Ser Phe Asn
145 150 155 160

Val Thr Thr Glu Val Ile Asn Lys Lys Lys Gln Glu His Ala Leu Phe
165 170 175

Tyr Lys Leu Asp Val Val Gln Met Asp Asp Asn Ser Thr Asn Thr Asn
180 185 190

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro
195 200 205

Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
210 215 220

Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro
225 230 235 240

Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val
245 250 255

Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile
260 265 270

Ile Ile Arg Ser Glu Asn Leu Thr Asn Asn Ala Lys Thr Ile Ile Val
275 280 285

Gln Leu Asn Glu Ser Val Pro Ile Asn Cys Ser Arg Pro Tyr Glu Asn
290 295 300

Lys Arg Arg Arg Thr Pro Ile Gly Leu Gly Gln Tyr Tyr Thr Thr Lys
305 310 315 320

Leu Lys Gly Tyr Ile Arg Pro Ala His Cys Asn Ile Ser Gly Ala Glu
325 330 335

Trp Asn Lys Thr Leu Gln Gln Val Ala Lys Lys Leu Gly Asp Leu Phe
340 345 350

Asn Gln Thr Thr Ile Ile Phe Gln Pro His Ser Gly Gly Asp Pro Glu
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp
370 375 380

Thr Ser Arg Leu Phe Asn Arg Thr Tyr Ser Thr Ser Gly Ser Thr Gly
385 390 395 400

Val Asn Asn Ser Thr Ile Lys Leu Pro Cys Arg Ile Lys Gln Ile Ile
405 410 415

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Glu
420 425 430

Gly Leu Ile Lys Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
435 440 445

Asp Gly Gly Asn Asn Thr Arg Gln Asn Glu Ala Phe Arg Pro Gly Gly
450 455 460

Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val
465 470 475 480

Val Arg Ile Glu Pro Leu Gly Leu Ala Pro Thr Glu Ala Lys Arg Arg
485 490 495

Val Val Glu Arg Glu Lys Arg Ala Ile Gly Leu Gly Ala Met Phe Leu
500 505 510

Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr
515 520 525

Leu Thr Val Gln Ala Arg Gln Leu Met Ser Gly Ile Val Gln Gln Gln
530 535 540

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr
545 550 555 560

Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu
565 570 575

Ser Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
580 585 590

Arg His Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser Asn
595 600 605

Lys Ser Leu Asn Glu Ile Trp Gly Asn Met Thr Trp Met Glu Trp Glu
610 615 620

Lys Glu Ile Asp Asn Tyr Thr Glu Leu Ile Tyr Ser Leu Ile Glu Glu
625 630 635 640

Ser Gln Thr Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Lys Leu Asp
645 650 655

Gln Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr Lys Trp Leu Trp
660 665 670

Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
675 680 685

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
690 695 700

Ser Pro Leu Ser Phe Gln Thr Leu Leu Pro Ala Pro Arg Gly Pro Asp
705 710 715 720

Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Gln Gly Arg Gly Arg
725 730 735

Ser Ile Arg Leu Val Thr Gly Phe Ser Ala Leu Ile Trp Asp Asp Leu
740 745 750

Arg Asn Leu Cys Leu Phe Ser Tyr Arg His Leu Arg Asp Leu Ile Leu
755 760 765

Ile Ala Ala Lys Ile Val Glu Phe Leu Gly Arg Arg Gly
770 775 780

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<211> 2586
<212> DNA
<213> HIV-1

<400> 11
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gtacctgtgt ggaaagatgc agaaaccacc ttattttgtg catcagatgc gaaagcatat 180

gatacagaag tgcataatgt ctggggccaca catgcctgtg tacctacaga ccccaaccca	240
caagaaataa atttggaaaa tgtgacagaa aattttaaca tgtggaaaaa taacatggta	300
gagcagatgc atacagatat aatcagtcta tgggaccaa gcctaaagcc atgtgtacag	360
ttaacccctc tctgtgttac tttagattgt actgatgcca caaatgccac taataccact	420
atcattagt acatgaaagg agaaataaaa aactgctctt tcaatatgac cacagaatta	480
aaggataaga cacagaaagt acgttcattt ttctataaga tggatatagt acaaattaac	540
aacaacaaca gcaacagcaa cagtagtcag tatagattaa taagttgtaa tacctcaacc	600
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ataatagggg atataagaca agcacattgt aacatcagta gagcagcatg gaataacact	1020
ttgcagaagg tagcccaaca attaagaaca cactttgaga acagaacaat aatctttaat	1080
cactccgcag gaggggaccc agaaataact acacatagtt ttaattgtgg aggagaattt	1140
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agatgtgact caaacattac aggactaata ttaacaagag atggggggga taataacagc	1380
acaaatgaga ccttcagacc tggaggagga gatatgaggg acaattggag aagtgaatta	1440
tataagtata aagtagtaaa gattgaacca ctaggagtag caccaccag ggcaaagaga	1500
agagtgggtg aaagagaaaa aagagcaata gcaggaatag gagctgtgtt ccttgggttc	1560
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atttgcacca ctactgtgcc ctggaactct agttggagta ataaatccta tagtgagata	1860
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tatgatctaa ttgaagaatc acagaaccag caggaaaaga atgaacaaga cctattggca	1980
ttggacaagt gggcaaactc atggaattgg tttgacatat caaatggct gtggtatata	2040
agaatattta taatgatagt aggaggctta ataggattaa gaatagtttt tgctgtaatt	2100

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tcagtaataa atagagttag gcagggatac tcacctttgt cgttccagac ccttgccccg 2160
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caataa 2586

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<210> 12
<211> 861
<212> PRT
<213> HIV-1

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<400> 12

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Met Arg Val Lys Ile Gln Arg Asn Cys Gln Asn Leu Trp Arg Trp Gly
1          5          10          15

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Thr Ile Ile Leu Gly Met Met Ile Ile Cys Ser Ala Ala Glu Lys Leu
          20          25          30

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Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Glu Thr
          35          40          45

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Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
          50          55          60

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Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
          65          70          75          80

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Glu Ile Asn Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn
          85          90          95

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```

Asn Met Val Glu Gln Met His Thr Asp Ile Ile Ser Leu Trp Asp Gln
          100          105          110

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Ser Leu Lys Pro Cys Val Gln Leu Thr Pro Leu Cys Val Thr Leu Asp
          115          120          125

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Cys Thr Asp Ala Thr Asn Ala Thr Asn Thr Thr Ile Ile Ser Asp Met
          130          135          140

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Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Lys
          145          150          155          160

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Asp Lys Thr Gln Lys Val Arg Ser Phe Phe Tyr Lys Met Asp Ile Val
165 170 175

Gln Ile Asn Asn Asp Asn Asn Ser Asn Ser Asn Ser Ser Gln Tyr Arg
180 185 190

Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
210 215 220

Ile Leu Lys Cys Lys Asp Lys Glu Phe Asn Gly Thr Gly Pro Cys Arg
225 230 235 240

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser
245 250 255

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Lys Val Met Ile
260 265 270

Arg Ser Glu Asn Ile Thr Asp Asn Thr Lys Asn Ile Ile Val Gln Leu
275 280 285

Thr Glu Pro Val Lys Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
290 295 300

Arg Gly Ile Ser Ile Gly Pro Gly Arg Ala Phe Ile Ala Arg Asp Arg
305 310 315 320

Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Arg Ala Ala
325 330 335

Trp Asn Asn Thr Leu Gln Lys Val Ala Gln Gln Leu Arg Thr His Phe
340 345 350

Glu Asn Arg Thr Ile Ile Phe Asn His Ser Ala Gly Gly Asp Pro Glu
355 360 365

Ile Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Ser
370 375 380

Thr Thr Gly Leu Phe Asn Ser Thr Trp Ala Ser Asn Ala Ser Thr Gln
385 390 395 400

Gly Ser Asn Ser Thr Gly Ser Asn Asp Thr Ile Thr Leu Gln Cys Arg
405 410 415

Ile Arg Gln Ile Ile Arg Met Trp Gln Arg Val Gly Gln Ala Met Tyr
420 425 430

Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser Asn Ile Thr Gly
435 440 445

Leu Ile Leu Thr Arg Asp Gly Gly Asp Asn Asn Ser Thr Asn Glu Thr
450 455 460

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu
465 470 475 480

Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr
485 490 495

Arg Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Ile Ala Gly
500 505 510

Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met
515 520 525

Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Thr Arg Gln Leu Leu Ser
530 535 540

Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln
545 550 555 560

Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala
565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp
595 600 605

Asn Ser Ser Trp Ser Asn Lys Ser Tyr Ser Glu Ile Trp Asp Asn Met
610 615 620

Thr Trp Leu Gln Glu Trp Lys Glu Ile Ser Asn Tyr Thr Gln Ile Ile
625 630 635 640

Tyr Asp Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
645 650 655

Asp Leu Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp
660 665 670

Ile Ser Lys Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met Ile Val Gly
675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Ala Val Ile Ser Val Ile Asn
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Ala Pro
705 710 715 720

Asn Pro Gly Gly Leu Asp Arg Pro Gly Arg Ile Glu Glu Glu Gly Gly
725 730 735

Glu Gln Asp Arg Ser Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala
740 745 750

Leu Ala Trp Glu Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg
755 760 765

Leu Arg Asp Phe Ile Leu Ile Ala Ala Arg Thr Val Glu Leu Leu Gly
770 775 780

His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Glu Gly Leu Lys Tyr
785 790 795 800

Leu Gly Asn Leu Leu Leu Tyr Trp Gly Gln Glu Leu Lys Ile Ser Ala
805 810 815

Ile Ser Leu Phe Asp Thr Ile Ala Ile Val Ile Ala Gly Trp Thr Asp
820 825 830

Arg Val Ile Glu Ile Gly Gln Arg Ile Gly Arg Ala Ile Leu Asn Ile
835 840 845

Pro Arg Arg Ile Arg Gln Gly Ala Glu Arg Ala Leu Gln
850 855 860

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<211> 2607
<212> DNA
<213> HIV-1

<400> 13
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tatgatacag aggcacataa tgtttgggcc acacatgcct gtgtaccac agacccaac 240

ccacaagaaa tagtattggc aaatgtgaca gaagatttta acatgtggaa aaataacatg	300
gtagaacaga tgcattgagga tataatcagt ttatgggatc aaagcctaaa gccatgtgta	360
aaattaaccc cactctgtgt tactttaaat tgcactgatg taaggaatgg tactattgtg	420
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gatgtaatac caataggtaa tgataataat actaatacca gcaataataa tatcacctat	600
accagctata gggttgagaag ttgtaatacc tcagtcatta cacaggcctg tccaaagata	660
aactttgagc caattcccat acattattgt gccccggctg gggttgcgat tctgaagtgt	720
aataatagga cgttcgaggg aaaaggacca tgtaaaaatg tcagcacagt acaatgtaca	780
catggaatta ggccagtagt atcaactcaa ctgctgttaa atggcagtct agcagaaaaa	840
gatatagtaa ttagatctgc caatttctca gacaatgcta aagccataat agtacagctg	900
aacgaaactg tacaatatcaa ttgtacaaga cccaacaaca atacaagaag aagaataact	960
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gaaattgtaa tgcacagttt taattgtgga ggggaatttt tctactgtaa tacaacaaaa	1200
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gggctgctat taacaagaga tgggtggaat accaacgata ctaacaatac tgagatcttc	1440
agacctggag gaggagatat gagggacaat tggagaagtg aattatataa atataaagta	1500
gtaaaaattg aaccattagg aatagcacc accaaggcaa agagaagagt ggtgcaaaga	1560
gaaaaaagag caatgggaat aggagctctg ttccttgggt tcttgggagc agcaggaagc	1620
actatgggag cagcgtcaat gacgctgacg gtacaggcca gacaactatt gtctggtata	1680
gtgcaacagc agaacaattt gctgagggct attgaggcgc aacaccatct gttgcaactc	1740
acagtctggg gcatcaagca gctccaggca agagtcctgg ctgtggaaag atacctaaag	1800
gatcaacagc tcctggggat ttgggggttg tctggaaaac tcatttgcac cactgctgtg	1860
ccttggaatg ctagttggag taataaatct ctggataaga tttggaataa catgacctgg	1920
atgcagtggg aaagagaaat tgacaattac acaagtctaa tatacacttt aattgaagaa	1980
tcgcagaacc aacaagaaaa gaatgaacta gagttactag aattagataa atgggcaa	2040
ttgtggaatt gggttgacat aacaaaatgg ctgtggtata taaaaatatt cataatgata	2100
gtaggaggct tgatagggtt aagaatagtt tttgttatac tttctatagt gaatagagtt	2160

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aggcagggat actcaccatt atcgtttcag acccgctcc cagcccagag gggacccgac 2220
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<210> 14
<211> 866
<212> PRT
<213> HIV-1

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<400> 14

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Met Arg Val Lys Ile Lys Asn Tyr Gln His Leu Trp Arg Trp Ser Thr
1          5          10          15

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Met Leu Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu Gln Leu
          20          25          30

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```

Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Asn Thr
          35          40          45

```

```

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala His
          50          55          60

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Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
65          70          75          80

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Glu Ile Val Leu Ala Asn Val Thr Glu Asp Phe Asn Met Trp Lys Asn
          85          90          95

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Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
          100          105          110

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```

Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn
          115          120          125

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```

Cys Thr Asp Val Arg Asn Gly Thr Ile Val Arg Asn Ser Thr Ile Arg
          130          135          140

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```

Val Glu Glu Gly Met Lys Glu Glu Ile Lys Asn Cys Ser Phe Asn Val
145          150          155          160

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Thr Thr Ser Met Gly Asp Lys Leu Gln Lys Glu Asp Ala Phe Phe Tyr
 165 170 175
 Lys Ser Asp Val Val Gln Met Gly Asp Asn Asn Asn Thr Asn Thr Ser
 180 185 190
 Asn Asn Asn Ile Thr Tyr Thr Ser Tyr Arg Leu Arg Ser Cys Asn Thr
 195 200 205
 Ser Val Ile Thr Gln Ala Cys Pro Lys Ile Asn Phe Glu Pro Ile Pro
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 Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn
 225 230 235 240
 Arg Thr Phe Glu Gly Lys Gly Pro Cys Lys Asn Val Ser Thr Val Gln
 245 250 255
 Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn
 260 265 270
 Gly Ser Leu Ala Glu Lys Asp Ile Val Ile Arg Ser Ala Asn Phe Ser
 275 280 285
 Asp Asn Ala Lys Ala Ile Ile Val Gln Leu Asn Glu Thr Val Gln Ile
 290 295 300
 Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Arg Arg Ile Thr Met Gly
 305 310 315 320
 Pro Gly Ala Val Tyr Tyr Thr Thr Gly Asp Ile Ile Gly Asp Ile Arg
 325 330 335
 Arg Ala His Cys Asn Ile Ser Lys Glu Asp Trp Thr Asn Thr Leu Lys
 340 345 350
 Gln Ile Ala Lys Lys Leu Arg Glu Gln Phe Gly Asp Asn Lys Thr Ile
 355 360 365
 Ala Phe Lys Pro Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser
 370 375 380
 Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu Phe
 385 390 395 400
 Asn Ser Thr Trp Phe Gly Asn Ser Thr Arg Asn Asn Thr Glu Gly Ser
 405 410 415

Ser Asn Asn Gly Asn Ile Thr Leu Gln Cys Arg Ile Lys Gln Ile Ile
 420 425 430

Asn Met Trp Gln Gly Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg
 435 440 445

Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
 450 455 460

Asp Gly Gly Asn Thr Asn Asp Thr Asn Asn Thr Glu Ile Phe Arg Pro
 465 470 475 480

Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
 485 490 495

Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro Thr Lys Ala Lys
 500 505 510

Arg Arg Val Val Gln Arg Glu Lys Arg Ala Met Gly Ile Gly Ala Leu
 515 520 525

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser
 530 535 540

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
 545 550 555 560

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln His His Leu Leu
 565 570 575

Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala
 580 585 590

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
 595 600 605

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
 610 615 620

Ser Asn Lys Ser Leu Asp Lys Ile Trp Asn Asn Met Thr Trp Met Gln
 625 630 635 640

Trp Glu Arg Glu Ile Asp Asn Tyr Thr Ser Leu Ile Tyr Thr Leu Ile
 645 650 655

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Leu Glu Leu Leu Glu
 660 665 670

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Thr Lys Trp
 675 680 685
 Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly
 690 695 700
 Leu Arg Ile Val Phe Val Ile Leu Ser Ile Val Asn Arg Val Arg Gln
 705 710 715 720
 Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Gln Arg Gly
 725 730 735
 Pro Asp Arg Pro Glu Gly Ile Glu Glu Gly Gly Gly Arg Gly Arg
 740 745 750
 Asp Thr Ser Gly Pro Leu Val Asp Gly Phe Leu Ala Ile Ile Trp Val
 755 760 765
 Asp Leu Arg Ser Leu Phe Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
 770 775 780
 Leu Leu Ile Ala Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
 785 790 795 800
 Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ile Gln Glu
 805 810 815
 Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val
 820 825 830
 Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ala Arg Arg Thr Phe Arg
 835 840 845
 Ala Ile Leu His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala
 850 855 860
 Leu Leu
 865

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 <211> 2586
 <212> DNA
 <213> HIV-1

<400> 15
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 gtacctgtgt ggaaggaaac aaccaccact ctattttgtg catcagatgc taaagcatat 180

gataaagagg tacataatgt ttggggccaca catgcctgtg taccacaga cccaacca	240
caagaaatac cattggtaaa tgtaacagaa aattttaaca tgtggaaaaa taacatggta	300
gatcaaatgc atgaggatat aatcagttta tgggatcaaa gcctaaagcc atgtgtaaaa	360
ttaacccac tctgtgttac tttaaattgc actgatgatt tgaggaatgc tactaatacc	420
actactaata ccaatagtaa ttgggagaaa ccaatggaga aaggagaaat aaaaaactgc	480
tctttcaaaa tcacctcaag cataagagat aaggtagaca aacaatatgc acttttttat	540
agccttgatg tagtaccaat aaagaataac aataatatta gcaataagat tagatatagg	600
ttaagaagtt gtaacacctc agtcattaca caggcctgtc caaaggtaac ctttgagcca	660
attcccatc attattgtgc cccggctggg tttgcgattc taaaatgtaa tgataagaag	720
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ccagtagtat caactcaact actgttaaact ggcagtctag cagaagaaga ggtagtaatt	840
agatctgaaa atttcacaga caatgctaaa accataatag tacaactgaa agaccctgta	900
gaaatcaatt gtacaagacc caacagaaat gcatggaaag gcatacctat tggagtacca	960
gggagaaaat tctatgcaag aagaaacata acaggagata taagacaagc atattgtaac	1020
cttagtatag caaagtggaa taacacttta aaacagatag ttgaaaaatt aagattacat	1080
tttaaaaata aaacaatagt ctttaatagt tcctcagggg gggaccaga aattatactg	1140
cacagtttta attgtggagg ggaatttttc tattgtaatt caacaaaact gtttaatagt	1200
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gtagcaccca ccaaggcaaa gagaagagtg gtgcagagag aaaaagagc agtgggaata	1560
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aataaatctc tggataggat ttggaataat atgacctgga tggagtggga aagagaaatt	1920
gacaattaca caggcttaat atacaactta attgaagaat cgcaaacca acaagaaaag	1980
aatgaacaag aattattagc attagataaa tgggcaagtt tgtggaattg gtttgacata	2040
acaaactggc tgtggtatat aaaaatattc ataattgatag taggaggctt gataggttta	2100

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aacgccacag ccatagcagt agctgagggg acagataggg ttatagaaat attacaaaga 2520
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ctataa 2586

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<212> PRT
<213> HIV-1

<400> 16

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Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Ala Asp Gln Leu
20 25 30

Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Thr Thr Thr
35 40 45

Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys Glu Val His
50 55 60

Asn Val Trp Ala Thr Met Ala Cys Val Pro Thr Phe Pro Asn Pro Gln
65 70 75 80

Ile Val Glu Asn Phe Asn Met Leu Lys Asn Asn Met Val Glu Gln Asp
85 90 95

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Thr
100 105 110

Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr Asp Asp Leu Arg
115 120 125

Asn Ala Asn Asn Thr Thr Thr Asn Thr Asn Ser Asn Trp Glu Lys Pro
130 135 140

Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile Thr Ser Ser
145 150 155 160

Ile Arg Asp Lys Val Gln Lys Gln Tyr Ala Leu Phe Tyr Ser Leu Asp
165 170 175

Val Val Pro Ile Lys Asn Asn Asn Asn Ile Ser Asn Lys Ile Arg Tyr
180 185 190

Arg Leu Arg Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
195 200 205

Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
210 215 220

Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Asn Val Val
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
260 265 270

Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln
275 280 285

Leu Lys Asp Pro Val Glu Ile Asn Cys Thr Arg Pro Asn Arg Asn Ala
290 295 300

Trp Lys Gly Ile Pro Ile Gly Val Pro Gly Arg Lys Phe Tyr Ala Arg
305 310 315 320

Arg Asn Ile Thr Gly Asp Ile Arg Gln Ala Tyr Cys Asn Leu Ser Ile
325 330 335

Ala Lys Trp Thr Asn Thr Leu Lys Gln Ile Val Glu Lys Leu Arg Leu
340 345 350

His Phe Lys Asn Lys Thr Ile Val Phe Lys Ser Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Ile Leu His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Lys Leu Phe Asn Ser Thr Trp Phe Ser Thr Thr Glu
385 390 395 400

Gly Leu Asn Asn Thr Gly Asn Glu Asp Pro Ile Val Leu Pro Cys Arg
405 410 415

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr
420 425 430

Ala Pro Pro Ile Ala Asp Leu Ile Arg Cys Ser Ser Asn Ile Thr Gly
435 440 445

Leu Leu Leu Thr Arg Asp Gly Gly Val Asp Glu Asn Ser Asn Thr Thr
450 455 460

Glu Thr Phe Arg Pro Gly Gly Gly Asn Met Arg Asp Asn Trp Arg Ser
465 470 475 480

Glu Leu Tyr Lys Tyr Lys Ala Val Lys Ile Glu Pro Leu Gly Val Ala
485 490 495

Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val
500 505 510

Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr
515 520 525

Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu
530 535 540

Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala
545 550 555 560

Gln Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln
565 570 575

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
580 585 590

Gly Phe Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
595 600 605

Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Arg Ile Trp Asn Asn
610 615 620

Met Thr Trp Met Glu Trp Glu Arg Glu Ile Asp Asn Tyr Thr Gly Leu
625 630 635 640

Ile Tyr Asn Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
645 650 655

Gln Glu Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
660 665 670

Asp Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val
675 680 685

Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val
690 695 700

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His His
705 710 715 720

Pro Ala Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Gly Glu Gly
725 730 735

Gly Glu Arg Asp Arg Asp Arg Ser Gly Pro Leu Val Asp Gly Phe Leu
740 745 750

Ala Ile Ile Trp Val Asp Leu Arg Ser Leu Cys Ile Phe Leu Tyr His
755 760 765

Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu
770 775 780

Gly Arg Arg Gly Trp Glu Val Leu Lys Tyr Trp Trp Asn Leu Leu Gln
785 790 795 800

Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Ile Asn Leu Leu Asn Ala
805 810 815

Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Ile Leu
820 825 830

Gln Arg Ala Phe Arg Ala Ile Leu His Ile Pro Thr Arg Ile Arg Gln
835 840 845

Gly Leu Glu Arg Ala Leu Leu
850 855

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<211> 2571
<212> DNA
<213> HIV-1

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gttcctgtgt ggagagaagc aacaaccact ctattctgtg catcagattc taaagcatat 180
gatacagagg cacataatgt ttgggccaca catgcctgtg taccacaga cccaaccca 240

caagaagtat tattggaaaa tgtgacagaa aattttaaca tgtggaaaaa tgacatggta	300
gaacagatgc atgaggatat aatcagtcta tgggatcaaa gcctaaagcc atgtgtaaaa	360
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<212> PRT
<213> HIV-1

<400> 18

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Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu Ala Thr Thr Thr
35 40 45

Leu Phe Cys Ala Ser Asp Ser Lys Ala Tyr Asp Thr Glu Ala His Asn
50 55 60

Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu
65 70 75 80

Val Leu Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp
85 90 95

Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser
100 105 110

Leu Lys Pro Cys Val Lys Leu Thr Pro Arg Cys Val Thr Leu Lys Cys
115 120 125

Thr Asp Tyr Glu Gly Asn Ala Asn Asn Thr Ile Asp Asn Ala Thr Lys
130 135 140

Asn Ser Trp Lys Gly Glu Ile Lys Asn Cys Thr Phe Asn Val Thr Thr
145 150 155 160

Ala Ile Arg Asp Lys Val Lys Lys Gln Tyr Ala Leu Phe His Ser Leu
165 170 175

Asp Val Val Pro Ile Lys Asp Ala Lys Asp Ser Asn Ser Tyr Arg Leu
180 185 190

Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val Ser
195 200 205

Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile
210 215 220

Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Lys Gly Gln Cys Lys Asn
225 230 235 240

Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Ala Ser Thr
245 250 255

Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Asp Ile Ile Ile Arg
260 265 270

Ser Asp Asn Phe Ser Asp Asn Ala Lys Ile Ile Ile Val Gln Leu Lys
275 280 285

Glu Pro Val Glu Ile Asn Cys Thr Arg Pro Gly Asn Asn Thr Arg Lys
290 295 300

Ser Ile His Ile Gly Pro Gly Arg Ala Trp Tyr Ala Thr Gly Asp Ile
305 310 315 320

Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Ser Val Lys Trp
325 330 335

Asn Asn Thr Leu Arg Gln Ile Ala Lys Lys Leu Gly Glu Gln Phe Gln
340 345 350

Asp Lys Asn Ile Thr Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile
355 360 365

Val Met His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ala
370 375 380

Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Gly Thr Trp Asn Asn Ser
385 390 395 400

Thr Trp Asn Glu Thr Asp Thr Thr Thr Ile Thr Leu Pro Cys Arg Ile
405 410 415

Lys Gln Ile Val Asn Met Trp Gln Thr Val Gly Arg Ala Met Tyr Ala
420 425 430

Pro Pro Ile Arg Gly Glu Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu
 435 440 445

Leu Leu Thr Arg Asp Gly Gly Asn Ile Asn Glu Thr Asn Gly Thr Glu
 450 455 460

Ile Phe Arg Pro Ala Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu
 465 470 475 480

Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Ile Ala Pro
 485 490 495

Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly
 500 505 510

Val Gly Ala Met Phe Leu Gly Phe Leu Ser Ala Ala Gly Ser Thr Met
 515 520 525

Gly Ala Ala Ser Val Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser
 530 535 540

Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln
 545 550 555 560

Gln His Leu Leu Gln Thr Leu Val Trp Gly Ile Lys Gln Leu Gln Ala
 565 570 575

Arg Val Leu Ala Val Glu Arg Tyr Leu Gly Asp Gln Gln Leu Leu Gly
 580 585 590

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp
 595 600 605

Asn Thr Ser Trp Ser Asn Lys Ser Leu Lys Tyr Ile Trp Asp Asn Met
 610 615 620

Thr Trp Met Gln Trp Asp Lys Glu Ile Ser Asn Tyr Thr Gly Leu Ile
 625 630 635 640

Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys
 645 650 655

Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp
 660 665 670

Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Ile Ile Val Gly
 675 680 685

Gly Leu Ile Gly Leu Arg Ile Val Phe Thr Val Leu Ser Ile Val Asn
690 695 700

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro
705 710 715 720

Thr Gln Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly
725 730 735

Glu Arg Asp Arg Asp Arg Ser Arg Thr Ser Val Asp Gly Phe Leu Ala
740 745 750

Leu Ile Trp Val Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg
755 760 765

Leu Arg Asp Leu Leu Leu Ile Leu Ala Arg Ile Val Glu Leu Leu Gly
770 775 780

Arg Arg Gly Trp Glu Thr Leu Arg Tyr Trp Trp Asn Leu Leu Gln Tyr
785 790 795 800

Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn Ser Ile
805 810 815

Ala Ile Val Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln
820 825 830

Arg Val Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg Gln Gly
835 840 845

Leu Glu Arg Ala Leu Leu
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<210> 19
<211> 2589
<212> DNA
<213> HIV-1

<400> 19
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gtacccgtgt ggaaagaagc aaccaccact ctattctgtg catctgatgc taaagcatat 180
gatacagaga aacataatgt ttggggccaca catgcctgtg tacctacaga cccaaccca 240
caagaagtag tattggaaaa tgtgacagaa aattttaaca tgtggaaaaa taacatggta 300
gaacagatgc atgaggatat aatcagttta tgggatcaaa gtctaaagcc atgtgtaaaa 360

ctaaccacac	tctgtgtcac	tttaaactgt	aggaaacgtta	ctattacca	tactactacc	420
aatagtagtg	gctggaaact	aatggaggaa	ggagaaataa	aaaactgctc	tttcaaaatc	480
accacaatac	tgagacataa	gatgcaggaa	gaacatgcac	ttttttataa	atcagatgta	540
gtaccactag	gtaataatag	tgcaataggt	aataataatg	ccagatatag	gttgataagt	600
tgtaacacct	caaccattac	acaggcctgt	ccaaagggtat	cctttgagcc	aattcccata	660
cattattgtg	ccccggctgg	ttttgcgatt	ctaaaatgta	gagataagaa	gttcaatgga	720
acaggaccat	gtaaagatgt	cagcacagta	caatgtacac	atggaattaa	gccagtagta	780
tcaactcaac	tactgttaaa	tggcagtcta	gcagaagaag	atatagtaat	tagatctgcc	840
aattttctcag	acaatgctaa	aatcataata	gtacagctga	ataaaactgt	agtaattaat	900
tgtacaagac	ccaacaataa	tacaagaaaa	ggtataaata	taggaccagg	aagaacagtt	960
tatgcaacag	gaaaaataat	aggagatata	agacaagcac	attgtaacat	tagtaaagga	1020
gaatggtata	acacttttaa	gcaggtagtt	acaaaattag	gagaacattt	taagaataaa	1080
acaatagcct	ttaataaatc	ctcaggaggg	gaccagaaa	ttgtaaagca	cacttttaat	1140
tgtggagggg	aatttttcta	ctgtgattca	acaaaattgt	ttactagtac	ttggaactat	1200
actaatggta	cttggaatag	tactaactgg	aatgatactg	aaatgttgaa	taaaacaatc	1260
acactcccat	gcagaataaa	acaaattgta	aacatgtggc	aggaaagtagg	gaaagcaatg	1320
tatgcccctc	ccatcagcgg	acttattaca	tgttcatcaa	atattacagg	actactatta	1380
acaagagatg	gtggtagtaa	cacgaacacc	accgaggtct	tcagacctgg	aggaggaaat	1440
atgaaggaca	attggagaag	tgaattatat	aaatataaag	tagtaaaaaat	tgaaccatta	1500
ggagtagcac	ccaccaaggc	aaaaagaaga	gtgggtgcaga	gagaaaaaag	agcagtggga	1560
ataggagctc	tgttccttgg	gttcttggga	gcagcaggaa	gcactatggg	cgcagcgtca	1620
ctgacgctga	cggtagacag	cagacaatta	ttgtctggta	tagtgcagca	gcagaacaat	1680
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atttgggggt	gctctggaaa	actcatttgc	accactactg	tgcttggaa	tgctagttagg	1860
agtaataaat	ctctggatga	tatttggcag	aacatgacct	ggatggagtg	ggaaagagaa	1920
attgacaatt	acacaaatgt	aatatacaat	ttaattgaag	aatcgcagaa	ccagcaagaa	1980
aagaatgaac	aagacttatt	agcattggat	aaatgggcaa	gtttgtggga	ttggtttagc	2040
atatcaaact	ggctgtggta	tataaaaata	ttcataatga	tagtaggagg	cttgataggt	2100
ttaagaataa	tttttactgt	actttctata	gtgaatagag	ttaggcaggg	atactacca	2160
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 tattggtgga atctcctgca gtattggagt caggaactaa agaatagtgc tgtagcttg 2460
 cttaatgtca cagccatagc agtagctgag gggacagata ggattctaga agtattacaa 2520
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<210> 20
 <211> 862
 <212> PRT
 <213> HIV-1

<400> 20

Met Arg Val Lys Glu Ile Met Lys Asn Tyr Gln His Trp Trp Arg Gly
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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Lys
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Arg Asn Val Thr Ile Thr Asn Thr Thr Thr Asn Ser Ser Gly
130 135 140

Trp Lys Leu Met Glu Glu Gly Glu Ile Lys Asn Cys Ser Phe Lys Ile
145 150 155 160

Thr Thr Ile Leu Arg His Lys Met Gln Glu Glu His Ala Leu Phe Tyr
165 170 175

Lys	Ser	Asp	Val	Val	Pro	Leu	Gly	Asn	Asn	Ser	Ala	Ile	Gly	Asn	Asn	
			180					185					190			
Asn	Ala	Arg	Tyr	Arg	Leu	Ile	Ser	Cys	Asn	Thr	Ser	Thr	Ile	Thr	Gln	
		195					200					205				
Ala	Cys	Pro	Lys	Val	Thr	Phe	Glu	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	
	210					215					220					
Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Arg	Asp	Lys	Lys	Phe	Asn	Gly	
225					230					235					240	
Thr	Gly	Pro	Cys	Lys	Asp	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	
				245					250					255		
Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	
			260					265					270			
Glu	Asp	Ile	Val	Ile	Arg	Ser	Ala	Asn	Phe	Ser	Asp	Asn	Ala	Lys	Ile	
		275					280					285				
Ile	Ile	Val	Gln	Leu	Asn	Lys	Thr	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	
	290					295					300					
Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	Asn	Ile	Gly	Pro	Gly	Arg	Thr	Val	
305					310					315					320	
Tyr	Ala	Thr	Gly	Lys	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	
				325				330						335		
Ile	Ser	Lys	Gly	Glu	Trp	Tyr	Asn	Thr	Leu	Lys	Gln	Val	Val	Thr	Lys	
			340					345					350			
Leu	Gly	Glu	His	Phe	Lys	Asn	Lys	Thr	Ile	Ala	Phe	Asn	Lys	Ser	Ser	
		355					360					365				
Gly	Gly	Asp	Pro	Glu	Ile	Val	Lys	His	Thr	Phe	Asn	Cys	Gly	Gly	Glu	
	370					375					380					
Phe	Phe	Tyr	Cys	Asp	Ser	Thr	Lys	Leu	Phe	Thr	Ser	Thr	Trp	Asn	Tyr	
385					390					395					400	
Thr	Asn	Gly	Thr	Trp	Asn	Ser	Thr	Asn	Trp	Asn	Asp	Thr	Glu	Met	Leu	
				405					410					415		
Asn	Lys	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Val	Asn	Met	
			420					425					430			

Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Leu
 435 440 445

Ile Thr Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
 450 455 460

Gly Ser Asn Thr Asn Thr Thr Glu Val Phe Arg Pro Gly Gly Gly Asn
 465 470 475 480

Met Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
 485 490 495

Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val
 500 505 510

Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe
 515 520 525

Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr
 530 535 540

Val Gln Thr Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
 545 550 555 560

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Thr Leu Val
 565 570 575

Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr
 580 585 590

Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu
 595 600 605

Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser
 610 615 620

Leu Asp Asp Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg Glu
 625 630 635 640

Ile Asp Asn Tyr Thr Asn Val Ile Tyr Asn Leu Ile Glu Glu Ser Gln
 645 650 655

Asn Gln Gln Glu Lys Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp
 660 665 670

Ala Ser Leu Trp Asp Trp Phe Ser Ile Ser Asn Trp Leu Trp Tyr Ile
 675 680 685

Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile
 690 695 700
 Phe Thr Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro
 705 710 715 720
 Leu Ser Phe Gln Thr Arg Phe Pro Ala Pro Arg Gly Pro Asp Arg Pro
 725 730 735
 Glu Gly Ile Glu Glu Gly Gly Gly Glu Lys Asp Arg Asp Arg Ser Gly
 740 745 750
 Leu Leu Val Asn Gly Phe Phe Ala Leu Ile Trp Val Asp Leu Arg Ser
 755 760 765
 Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala
 770 775 780
 Ala Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ile Leu Lys
 785 790 795 800
 Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser
 805 810 815
 Ala Val Ser Leu Leu Asn Val Thr Ala Ile Ala Val Ala Glu Gly Thr
 820 825 830
 Asp Arg Ile Leu Glu Val Leu Gln Arg Ala Tyr Arg Ala Ile Ile His
 835 840 845
 Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu
 850 855 860

<210> 21

<211> 2598

<212> DNA

<213> HIV-1

<400> 21

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gtgtggagag acgcagagac caccttattt tgtgcatcag atgctaaagc atatgataca	180
gaagtacata atgtttgggc tacacatgcc tgtgtacca cagaccctaa cccacaagaa	240
atacctttgg aaaatgtaac agaaaatttt aatatgtgga aaaataacat ggtagagcag	300

gagcaagaca gagacaggtc cgtgagatta gtgaacggat tcttagctct tgcctgggac 2280
gatctacgga gcctgtgcct cttcagctac caccgattga gagacttact cttgattgca 2340
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gccctcaa atctgtggaa tcttctgtca tactggggcc aggaactaaa gaatagtgtc 2460
attaatctgc ttgatacaac agcaatagca gtagctaatt ggacagacag agttatagaa 2520
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<210> 22
<211> 864
<212> PRT
<213> HIV-1

<400> 22

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Ile	Ile	Phe	Trp	Ile	Met	Val	Ile	Cys	Asn	Ala	Glu	Asn	Leu	Trp	Val
			20					25					30		
Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Arg	Asp	Ala	Glu	Thr	Thr	Leu
		35					40					45			
Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Val	His	Asn	Val
	50					55					60				
Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Phe	Pro	Asn	Pro	Gln	Glu	Ile
65					70				75						80
Pro	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	Trp	Lys	Asn	Asn	Met
				85					90					95	
Val	Glu	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Asp	Trp	Asp	Gln	Ser	Leu
			100					105					110		
Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu	Asn	Cys	Thr
		115					120					125			
His	Asn	Phe	Asn	Asn	Phe	Asn	Ser	Ser	Asn	Asn	Ser	Thr	Pro	Ile	Asn
	130					135					140				
Asn	Thr	Ile	Tyr	Asn	Gly	Met	Gln	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe
145					150					155					160
Asn	Thr	Thr	Thr	Glu	Leu	Arg	Gly	Lys	Thr	Lys	Lys	Gln	Tyr	Ala	Leu

175

Ile Asn Gly Thr Asn His Thr Gly Pro Tyr Asp Thr Asp Thr Ile Thr
405 410 415

Leu Arg Cys Arg Ile Lys Gln Ile Val Lys Thr Trp Gln Arg Val Gly
 420 425 430
 Gln Ala Met Tyr Ala Pro Pro Ile Pro Gly Val Ile Arg Cys Asp Ser
 435 440 445
 Asn Ile Thr Gly Ile Leu Leu Thr Arg Asp Gly Gly Lys Ile Asn Ser
 450 455 460
 Thr Asn Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp
 465 470 475 480
 Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly
 485 490 495
 Val Ala Pro Thr His Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg
 500 505 510
 Ala Val Gly Val Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala
 515 520 525
 Gly Ser Thr Met Gly Ala Ala Ala Ile Thr Leu Thr Val Gln Ala Arg
 530 535 540
 Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala
 545 550 555 560
 Ile Glu Ala Gln Gln His Leu Leu Lys Thr Leu Val Trp Gly Ile Lys
 565 570 575
 Gln Leu Gln Ala Arg Val Leu Ala Leu Glu Arg Tyr Leu Arg Asp Gln
 580 585 590
 Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr
 595 600 605
 Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Thr Phe Asn Asp Ile
 610 615 620
 Trp Asn Met Thr Trp Leu Gln Trp Asp Lys Glu Ile Asn Asn Tyr Thr
 625 630 635 640
 Asn Thr Ile Tyr Arg Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys
 645 650 655
 Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Ser
 660 665 670

Trp Phe Asp Leu Ser Asn Trp Leu Trp Tyr Ile Arg Ile Phe Ile Met
 675 680 685
 Val Val Gly Gly Leu Ile Ala Leu Arg Ile Val Phe Ala Val Leu Ala
 690 695 700
 Ile Ile Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr
 705 710 715 720
 Leu Thr His His Gln Arg Glu Pro Asp Arg Pro Glu Gly Ile Glu Glu
 725 730 735
 Gly Gly Gly Glu Gln Asp Arg Asp Arg Ser Val Arg Leu Val Asn Gly
 740 745 750
 Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser
 755 760 765
 Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Ala Ala Arg Thr Val Glu
 770 775 780
 Leu Leu Gly His Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Gly Ala
 785 790 795 800
 Leu Lys Tyr Leu Trp Asn Leu Leu Ser Tyr Trp Gly Gln Glu Leu Lys
 805 810 815
 Asn Ser Ala Ile Asn Leu Leu Asp Thr Thr Ala Ile Ala Val Ala Asn
 820 825 830
 Trp Thr Asp Arg Val Ile Glu Ile Gly Gln Arg Phe Gly Arg Ala Ile
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 Leu Asn Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Gln
 850 855 860

<210> 23
 <211> 24
 <212> DNA
 <213> Primer

<400> 23
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24

<210> 24
 <211> 24
 <212> DNA
 <213> Primer

<400> 24
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24

<210> 25
<211> 25
<212> DNA
<213> Primer

<400> 25
gagacagtgg caatgagagt gaagg

25

<210> 26
<211> 26
<212> DNA
<213> Primer

<400> 26
ctttttgacc acttgccacc catctt

26

<210> 27
<211> 7
<212> PRT
<213> Peptide

<400> 27

His Ser Ser Leu Lys Gly Leu
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